

ABSTRACT OF THE DISCLOSURE

In automatically designing a base sequence to be used as a probe which is hybridized with an unknown nucleic acid fragment to perform gene analysis, a discrimination tree in which a plurality of partial base sequences obtained from target base sequence data are arranged on nodes is generated. The suitability as a probe of a partial base sequence represented by a desired node is evaluated. A plurality of partial base sequences are grouped on the basis of specificity, and an appropriate group combination is selected. A partial base sequence to be used as a probe is determined, from partial base sequences belonging to the selected groups, on the basis of the evaluation result. In this manner, a probe appropriate for analysis can be automatically selected in accordance with a target base sequence to be analyzed. This effectively supports probe designing.

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